

L. Helms

1642Helms

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/038,261

DATE: 09/28/1999  
TIME: 15:04:12

INPUT SET: S33504.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ATTACHMENT  
TO  
#11

SEQUENCE LISTING

ENTERED

1  
2  
3 (1) General Information  
4  
5  
6 (i) APPLICANT: Reiter, Robert  
7 Witte, Owen  
8  
9 (ii) TITLE OF THE INVENTION: PSCA: Prostate Stem Cell Antigen  
10  
11  
12 (iii) NUMBER OF SEQUENCES: 7  
13  
14 (iv) CORRESPONDENCE ADDRESS:  
15 (A) ADDRESSEE: Mandel & Adriano  
16 (B) STREET: 35 N. Arroyo Parkway, Suite 60  
17 (C) CITY: Pasadena  
18 (D) STATE: California  
19 (E) COUNTRY: USA  
20 (F) ZIP: 91103  
21  
22 (v) COMPUTER READABLE FORM:  
23 (A) MEDIUM TYPE: Diskette  
24 (B) COMPUTER: IBM Compatible  
25 (C) OPERATING SYSTEM: DOS  
26 (D) SOFTWARE: FastSEQ for Windows Version 2.0  
27  
28 (vi) CURRENT APPLICATION DATA:  
29 (A) APPLICATION NUMBER: 09/038,261  
30 (B) FILING DATE: 10-MAR-1998  
31 (C) CLASSIFICATION:  
32  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 08/814,279  
35 (B) FILING DATE: 10-MAR-1997  
36  
37 (viii) ATTORNEY/AGENT INFORMATION:  
38 (A) NAME: Sarah B. Adriano  
39 (B) REGISTRATION NUMBER: 34,470  
40 (C) REFERENCE/DOCKET NUMBER: 30435.54USI2  
41  
42 (ix) TELECOMMUNICATION INFORMATION:  
43 (A) TELEPHONE: 626-395-7801  
44 (B) TELEFAX: 626-395-0694  
45 (C) TELEX:  
46

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47  
48 (2) INFORMATION FOR SEQ ID NO:1:  
49  
50 (i) SEQUENCE CHARACTERISTICS:  
51 (A) LENGTH: 998 base pairs  
52 (B) TYPE: nucleic acid  
53 (C) STRANDEDNESS: single  
54 (D) TOPOLOGY: linear  
55 (ii) MOLECULE TYPE: cDNA  
56 (ix) FEATURE:  
57  
58 (A) NAME/KEY: Other  
59 (B) LOCATION: 1...998  
60 (D) OTHER INFORMATION: Human PSCA nucleotide sequence  
61  
62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
63  
64 AGGGAGAGGC AGTGACCATG AAGGCTGTGC TGCTTGCCCT GTTGATGGCA GGCTTGCCCC 60  
65 TGCAGCCAGG CACTGCCCTG CTGTGCTACT CCTGCAAAGC CCAGGTGAGC AACGAGGACT 120  
66 GCCTGCAGGT GGAGAACTGC ACCCAGCTGG GGGAGCAGTG CTGGACCGCG CGCATCCGCG 180  
67 CAGTTGGCCT CCTGACCGTC ATCAGCAAAG GCTGCAGCTT GAACTGCGTG GATGACTCAC 240  
68 AGGACTACTA CGTGGGCAAG AAGAACATCA CGTGCTGTGA CACCGACTTG TGCAACGCCA 300  
69 GCGGGGCCCC TGCCCTGCAG CCGGCTGCCG CCATCCTTGC GCTGCTCCCT GCATCCGGCC 360  
70 TGCTGCTCTG GGGACCCGGC CAGCTATAGG CTCTGGGGGG CCCCCTGCA GCCCACTG 420  
71 GGTGTGGTGC CCCAGGCCTT TGTGCCATC CTCACAGAAC CTGGCCAGT GGGAGCCTGT 480  
72 CCTGGTTCCT GAGGCACATC CTAACGCAAG TTTGACCATG TATGTTTGCA CCCCTTTTCC 540  
73 CCNAACCCTG ACCTTCCCAT GGGCCTTTTC CAGGATTCCN ACCNGGCAGA TCAGTTTTAG 600  
74 TGANACANAT CCGCNTGCAG ATGGCCCTC CAACNNTTIN TGTTGNTGTT TCCATGGCCC 660  
75 AGCATTTTCC ACCCTTAACC CTGTGTTTCTG GCACTTNTTC CCCCAGGAAG CCTTCCCTGC 720  
76 CCACCCCAT TATGAATTGA GCCAGGTTTG GTCCGTGGTG TCCCCCGCAC CCAGCAGGGG 780  
77 ACAGGCAATC AGGAGGGCCC AGTAAAGGCT GAGATGAAGT GGACTGAGTA GAACTGGAGG 840  
78 ACAAGAGTTG ACGTGAGTTC CTGGGAGTTT CCAGAGATGG GGCCTGGAGG CCTGGAGGAA 900  
79 GGGGCCAGGC CTCACATTTG TGGGGNTCCC GAATGGCAGC CTGAGCACAG CGTAGGCCCT 960  
80 TAATAAACAC CTGTTGGATA AGCCAAAAA AAAAAAAA 998  
81  
82 (2) INFORMATION FOR SEQ ID NO:2:  
83  
84 (i) SEQUENCE CHARACTERISTICS:  
85 (A) LENGTH: 123 amino acids  
86 (B) TYPE: amino acid  
87 (C) STRANDEDNESS: unknown  
88 (D) TOPOLOGY: unknown  
89 (ii) MOLECULE TYPE: protein  
90 (ix) FEATURE:  
91  
92 (A) NAME/KEY: Other  
93 (B) LOCATION: 1...123  
94 (D) OTHER INFORMATION: Human PSCA amino acid sequence  
95  
96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
97  
98 Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln  
99 1 5 10 15

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100 Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn  
101 20 25 30  
102 Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys  
103 35 40 45  
104 Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys  
105 50 55 60  
106 Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly  
107 65 70 75 80  
108 Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly  
109 85 90 95  
110 Ala His Ala Leu Gln Pro Ala Ala Ile Leu Ala Leu Leu Pro Ala  
111 100 105 110  
112 Leu Gly Leu Leu Trp Gly Pro Gly Gln Leu  
113 115 120  
114

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 441 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...441

(D) OTHER INFORMATION: mPSCA nucleotide sequence

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

131 ATGAAGACAG TTTT TTTTAT CCTGCTGGCC ACCTACTTAG CCCTGCATCC AGGTGCTGCT 60  
132 CTGCAGTGCT ATTCATGCAC AGCACAGATG AACAAACAGAG ACTGTCTGAA TGTACAGAAC 120  
133 TGCAGCCTGG ACCAGCACAG TTGCTTTACA TCGCGCATCC GGGCCATTGG ACTCGTGACA 180  
134 GTTATCAGTA AGGGCTGCAG CTCACAGTGT GAGGATGACT CGGAGAACTA CTATTTGGGC 240  
135 AAGAAGAACA TCACGTGCTG CTA CTCTGAC CTGTGCAATG TCAACGGGGC CCACACCCTG 300  
136 AAGCCACCCA CCACCCTGGG GCTGCTGACC GTGCTCTGCA GCCTGTTGCT GTGGGGCTCC 360  
137 AGCCGTCTGT AGGCTCTGGG AGAGCCTACC ATAGCCCGAT TGTGAAGGGA TGAGCTGCAC 420  
138 TCCACCCAC CCCCACACAG G 441  
139

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: unknown

(D) TOPOLOGY: unknown

## (ix) FEATURE:

(A) NAME/KEY: Other

(B) LOCATION: 1...123

(D) OTHER INFORMATION: mPSCA amino acid translation

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153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
154  
155 Met Lys Thr Val Phe Phe Ile Leu Leu Ala Thr Tyr Leu Ala Leu His  
156 1 5 10 15  
157 Pro Gly Ala Ala Leu Gln Cys Tyr Ser Cys Thr Ala Gln Met Asn Asn  
158 20 25 30  
159 Arg Asp Cys Leu Asn Val Gln Asn Cys Ser Leu Asp Gln His Ser Cys  
160 35 40 45  
161 Phe Thr Ser Arg Ile Arg Ala Ile Gly Leu Val Thr Val Ile Ser Lys  
162 50 55 60  
163 Gly Cys Ser Ser Gln Cys Glu Asp Asp Ser Glu Asn Tyr Tyr Leu Gly  
164 65 70 75 80  
165 Lys Lys Asn Ile Thr Cys Cys Tyr Ser Asp Leu Cys Asn Val Asn Gly  
166 85 90 95  
167 Ala His Thr Leu Lys Pro Pro Thr Thr Leu Gly Leu Leu Thr Val Leu  
168 100 105 110  
169 Cys Ser Leu Leu Leu Trp Gly Ser Ser Arg Leu  
170 115 120  
171

172 (2) INFORMATION FOR SEQ ID NO:5:  
173

174 (i) SEQUENCE CHARACTERISTICS:

175 (A) LENGTH: 140 amino acids

176 (B) TYPE: amino acid

177 (C) STRANDEDNESS: unknown

178 (D) TOPOLOGY: unknown

179 (ix) FEATURE:  
180

181 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
182

183 Met Lys Ile Phe Leu Pro Val Leu Leu Ala Ala Leu Leu Gly Val Glu  
184 1 5 10 15  
185 Arg Ala Ser Ser Leu Met Cys Phe Ser Cys Leu Asn Gln Lys Ser Asn  
186 20 25 30  
187 Leu Tyr Cys Leu Lys Pro Thr Ile Cys Ser Asp Gln Asp Asn Tyr Cys  
188 35 40 45  
189 Val Thr Val Ser Ala Ser Ala Gly Ile Gly Asn Leu Val Thr Phe Gly  
190 50 55 60  
191 His Ser Leu Ser Lys Thr Cys Ser Pro Ala Cys Pro Ile Pro Glu Gly  
192 65 70 75 80  
193 Val Asn Val Gly Val Ala Ser Met Gly Ile Ser Cys Cys Gln Ser Phe  
194 85 90 95  
195 Leu Cys Asn Phe Ser Ala Ala Asp Gly Gly Leu Arg Ala Ser Val Thr  
196 100 105 110  
197 Leu Leu Gly Ala Gly Leu Leu Leu Ser Leu Leu Pro Ala Leu Leu Arg  
198 115 120 125  
199 Phe Gly Pro Leu Leu Leu Trp Gly Pro Gly Gln Leu  
200 130 135 140  
201

202 (2) INFORMATION FOR SEQ ID NO:6:  
203

204 (i) SEQUENCE CHARACTERISTICS:

205 (A) LENGTH: 123 amino acids

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206          (B) TYPE: amino acid
207          (C) STRANDEDNESS: unknown
208          (D) TOPOLOGY: unknown
209
210          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
211
212  Met Lys Ala Val Leu Leu Ala Leu Leu Met Ala Gly Leu Ala Leu Gln
213    1          5          10          15
214  Pro Gly Thr Ala Leu Leu Cys Tyr Ser Cys Lys Ala Gln Val Ser Asn
215          20          25          30
216  Glu Asp Cys Leu Gln Val Glu Asn Cys Thr Gln Leu Gly Glu Gln Cys
217          35          40          45
218  Trp Thr Ala Arg Ile Arg Ala Val Gly Leu Leu Thr Val Ile Ser Lys
219          50          55          60
220  Gly Cys Ser Leu Asn Cys Val Asp Asp Ser Gln Asp Tyr Tyr Val Gly
221          65          70          75          80
222  Lys Lys Asn Ile Thr Cys Cys Asp Thr Asp Leu Cys Asn Ala Ser Gly
223          85          90          95
224  Ala His Ala Leu Gln Pro Ala Ala Ala Ile Leu Ala Leu Leu Pro Ala
225          100          105          110
226  Leu Gly Leu Leu Leu Trp Gly Pro Gly Gln Leu
227          115          120
228
229          (2) INFORMATION FOR SEQ ID NO:7:
230
231          (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 123 amino acids
233          (B) TYPE: amino acid
234          (C) STRANDEDNESS: unknown
235          (D) TOPOLOGY: unknown
236
237          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
238
239  Met Lys Thr Val Leu Phe Leu Leu Leu Ala Thr Tyr Leu Ala Leu His
240    1          5          10          15
241  Pro Gly Ala Ala Leu Gln Cys Tyr Ser Cys Thr Ala Gln Met Asn Asn
242          20          25          30
243  Arg Asp Cys Leu Asn Val Gln Asn Cys Ser Leu Asp Gln His Ser Cys
244          35          40          45
245  Phe Thr Ser Arg Ile Arg Ala Ile Gly Leu Val Thr Val Ile Ser Lys
246          50          55          60
247  Gly Cys Ser Ser Gln Cys Glu Asp Asp Ser Glu Asn Tyr Tyr Leu Gly
248          65          70          75          80
249  Lys Lys Asn Ile Thr Cys Cys Tyr Ser Asp Leu Cys Asn Val Asn Gly
250          85          90          95
251

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/038,261**

DATE: 09/28/1999  
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*INPUT SET: S33504.raw*

Line

Error

Original Text